

BLAST Basic Local Alignment Search Tool

Job Title: lcI|31840 (21 letters) USSN 10/738,413

EXHIBIT 5

- Your search parameters were adjusted to search for a short input sequence.

Please, try our new design!

BLASTN 2.2.18+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402. RTD: 9HS90R0015 Database: human build 36.3 reference assembly genomic scaffolds 49,942 sequences; 5,818,011,736 total letters

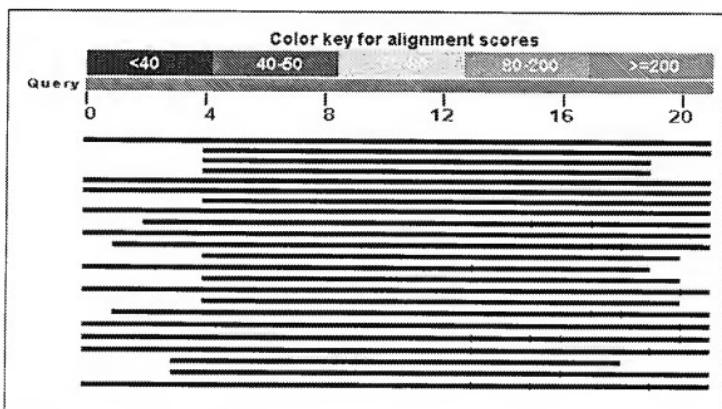
Genome View

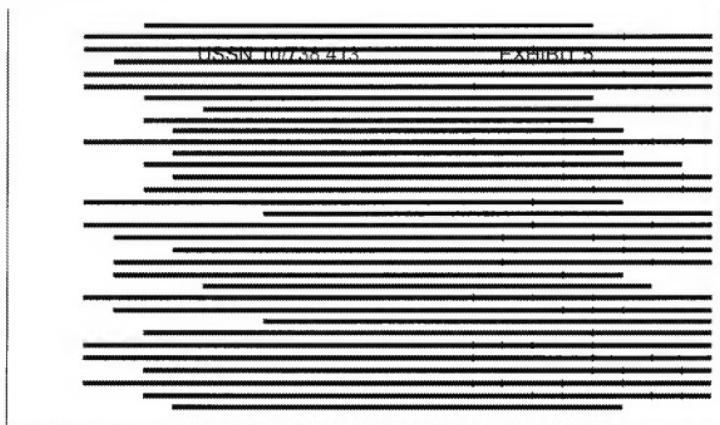
Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= Length=21

Designing or Testing PCR Primers? Try your s

Distribution of 654 Blast Hits on the Query Sequence





DISPLAY MODE: NEW

USSN 10/738.413

EXHIBIT 5

Legend for links to other resources: UniGene GEO Gene Structure Map

Sequences producing significant alignments:
(Click headers to sort columns)

Transcripts

| | | | | | | | | |
|--------------------------|--|------|------|------|-------|------|--|--|
| gi 113722118 NM_000372.4 | Homo sapiens tyrosinase (oculocutaneous albinism IA) (TYR), mRNA | 42.1 | 42.1 | 100% | 0.005 | 100% | | |
| gi 32313592 NM_006418.3 | Homo sapiens olfactomedin 4 (OLFM4), mRNA | 34.2 | 34.2 | 80% | 1.2 | 100% | | |
| gi 149363684 NM_015325.1 | Homo sapiens KIAA0947 protein (KIAA0947), mRNA | 30.2 | 30.2 | 71% | 19 | 100% | | |
| gi 142386366 NM_138392.2 | Homo sapiens SH3KBPI binding protein 1 (SHXKBPI), mRNA | 30.2 | 30.2 | 71% | 19 | 100% | | |

Genomic sequences [show first]

| | | | | | | | | |
|-----------------------------|---|------|------|------|-------|------|--|--|
| gi 157812179 NW_001838029.2 | Homo sapiens chromosome 11 genomic contig, alternate assembly (based on HuRef SCAF_1103279185367) | 42.1 | 42.1 | 100% | 0.005 | 100% | | |
| gi 51470779 NT_008984.17 | Homo sapiens chromosome 11 genomic contig, reference assembly | 42.1 | 42.1 | 100% | 0.005 | 100% | | |
| gi 157812202 NW_001838080.2 | Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188250) | 34.2 | 62.4 | 80% | 1.2 | 100% | | |
| gi 157697950 NW_001842360.1 | Homo sapiens chromosome X genomic contig, alternate assembly (based on HuRef SCAF_1103279188416) | 34.2 | 222 | 100% | 1.2 | 100% | | |
| gi 37546841 NT_024524.13 | Homo sapiens chromosome 13 genomic contig, reference assembly | 34.2 | 413 | 90% | 1.2 | 100% | | |
| gi 89059526 NT_011757.15 | Homo sapiens chromosome X genomic contig, reference assembly | 34.2 | 276 | 100% | 1.2 | 100% | | |
| gi 157696942 NW_001838065.1 | Homo sapiens chromosome 12 genomic contig, alternate assembly (based on HuRef SCAF_1103279188103) | 32.2 | 84.7 | 95% | 4.7 | 100% | | |
| gi 157811946 NW_001838849.2 | Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188271) | 32.2 | 58.5 | 76% | 4.7 | 100% | | |
| gi 157697620 NW_001838401.1 | Homo sapiens chromosome 16 genomic contig, alternate assembly (based on HuRef SCAF_1103279187672) | 32.2 | 58.5 | 90% | 4.7 | 100% | | |
| gi 157696568 NW_001839007.1 | Homo sapiens chromosome 7 genomic contig, alternate assembly (based on HuRef SCAF_1103279185597) | 32.2 | 58.5 | 76% | 4.7 | 100% | | |
| gi 157696481 NW_001838920.1 | Homo sapiens chromosome 4 | 32.2 | 84.7 | 100% | 4.7 | 100% | | |

genomic contig, alternate
assembly (based on HuRef
USSN107384183)

EXHIBIT 5

| | | | | | | |
|-----------------------------|--|------|------|------|-----|------|
| gi 37538184 NT_033968.5 | Homo sapiens chromosome 7 genomic contig, reference assembly | 32.2 | 58.5 | 76% | 4.7 | 100% |
| gi 89035805 NT_009755.18 | Homo sapiens chromosome 12 genomic contig, reference assembly | 32.2 | 252 | 95% | 4.7 | 100% |
| gi 88977422 NT_016354.18 | Homo sapiens chromosome 4 genomic contig, reference assembly | 32.2 | 403 | 100% | 4.7 | 100% |
| gi 88953723 NT_022135.15 | Homo sapiens chromosome 2 genomic contig, reference assembly | 32.2 | 220 | 100% | 4.7 | 100% |
| gi 51472974 NT_010393.15 | Homo sapiens chromosome 16 genomic contig, reference assembly | 32.2 | 428 | 100% | 4.7 | 100% |
| gi 157812194 NW_001838066.2 | Homo sapiens chromosome 12 genomic contig, alternate assembly (based on HuRef SCAF_1103279188213) | 30.2 | 30.2 | 71% | 19 | 100% |
| gi 157812193 NW_001838064.2 | Homo sapiens chromosome 12 genomic contig, alternate assembly (based on HuRef SCAF_1103279188390) | 30.2 | 111 | 85% | 19 | 100% |
| gi 157812275 NW_001838218.2 | Homo sapiens chromosome 15 genomic contig, alternate assembly (based on HuRef SCAF_1103279188258) | 30.2 | 351 | 100% | 19 | 100% |
| gi 157812414 NW_001838483.2 | Homo sapiens chromosome 19 genomic contig, alternate assembly (based on HuRef SCAF_1103279188176) | 30.2 | 30.2 | 71% | 19 | 100% |
| gi 157812175 NW_001838022.2 | Homo sapiens chromosome 11 genomic contig, alternate assembly (based on HuRef SCAF_1103279188392) | 30.2 | 399 | 100% | 19 | 100% |
| gi 157697854 NW_001838666.1 | Homo sapiens chromosome 20 genomic contig, alternate assembly (based on HuRef SCAF_1103279188360) | 30.2 | 58.5 | 100% | 19 | 100% |
| gi 157811963 NW_001838884.2 | Homo sapiens chromosome 3 genomic contig, alternate assembly (based on HuRef SCAF_1103279188385) | 30.2 | 508 | 95% | 19 | 100% |
| gi 157697894 NW_001838706.1 | Homo sapiens chromosome 21 genomic contig, alternate assembly (based on HuRef SCAF_1103279188379) | 30.2 | 244 | 100% | 19 | 100% |
| gi 157811817 NW_001838533.2 | Homo sapiens chromosome 1 genomic contig, alternate assembly (based on HuRef SCAF_1103279188157) | 30.2 | 375 | 100% | 19 | 100% |
| gi 157812405 NW_001838466.2 | Homo sapiens chromosome 18 genomic contig, alternate assembly (based on HuRef SCAF_1103279188324) | 30.2 | 30.2 | 71% | 19 | 100% |
| gi 157812170 NW_001838005.2 | Homo sapiens chromosome 10 genomic contig, alternate assembly (based on HuRef | 30.2 | 56.5 | 80% | 19 | 100% |

| | | | | | | | |
|-----------------------------|--|---------------------|------|------|----|------|-----------|
| | | SCAF_1103279188123) | | | | | |
| gi 157697891 NW_001838703.1 | Homo sapiens chromosome 21 genomic contig, alternate assembly (based on HuRef SCAF_1103279188184) | 30.2 | 30.2 | 71% | 19 | 100% | EXHIBIT 5 |
| gi 157696803 NW_001839242.1 | Homo sapiens chromosome 9 genomic contig, alternate assembly (based on HuRef SCAF_1103279188125) | 30.2 | 30.2 | 71% | 19 | 100% | |
| gi 157697933 NW_001838745.1 | Homo sapiens chromosome 22 genomic contig, alternate assembly (based on HuRef SCAF_1103279188372) | 30.2 | 32.5 | 100% | 19 | 100% | |
| gi 157812071 NW_001839109.2 | Homo sapiens chromosome 8 genomic contig, alternate assembly (based on HuRef SCAF_1103279182719) | 30.2 | 30.2 | 71% | 19 | 100% | |
| gi 157812219 NW_001838113.2 | Homo sapiens chromosome 14 genomic contig, alternate assembly (based on HuRef SCAF_1103279188183) | 30.2 | 139 | 85% | 19 | 100% | |
| gi 157811769 NW_001838589.2 | Homo sapiens chromosome 1 genomic contig, alternate assembly (based on HuRef SCAF_1103279188310) | 30.2 | 161 | 85% | 19 | 100% | |
| gi 157696564 NW_001839003.1 | Homo sapiens chromosome 7 genomic contig, alternate assembly (based on HuRef SCAF_1103279188377) | 30.2 | 294 | 90% | 19 | 100% | |
| gi 157697730 NW_001838329.1 | Homo sapiens chromosome 16 genomic contig, alternate assembly (based on HuRef SCAF_1103279188231) | 30.2 | 82.8 | 85% | 19 | 100% | |
| gi 157696323 NW_001838762.1 | Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279187945) | 30.2 | 30.2 | 71% | 19 | 100% | |
| gi 157812368 NW_001838328.2 | Homo sapiens chromosome 16 genomic contig, alternate assembly (based on HuRef SCAF_1103279187671) | 30.2 | 167 | 100% | 19 | 100% | |
| gi 157811893 NW_001838818.2 | Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188423) | 30.2 | 222 | 95% | 19 | 100% | |
| gi 157812178 NW_001838028.2 | Homo sapiens chromosome 11 genomic contig, alternate assembly (based on HuRef SCAF_1103279187758) | 30.2 | 82.8 | 85% | 19 | 100% | |
| gi 157696534 NW_001838973.1 | Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279188126) | 30.2 | 193 | 95% | 19 | 100% | |
| gi 157696439 NW_001838878.1 | Homo sapiens chromosome 3 genomic contig, alternate assembly (based on HuRef SCAF_1103279188187) | 30.2 | 56.5 | 80% | 19 | 100% | |
| gi 157696487 NW_001838926.1 | Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279187504) | 30.2 | 30.2 | 71% | 19 | 100% | |
| gi 157811959 NW_001838877.2 | | 30.2 | 399 | 100% | 19 | 100% | |

Homo sapiens chromosome 3
genomic contig, alternate
USGS|10|738|413 on HuRef
SCAF_1103279108143)

EXHIBIT 5

| | | | | | | |
|-----------------------------|---|------|------|------|----|------|
| gi 157697822 NW_001838484.1 | Homo sapiens chromosome 19 genomic contig, alternate assembly (based on HuRef SCAF_1103279188355) | 30.2 | 214 | 95% | 19 | 100% |
| gi 157696988 NW_001838110.1 | Homo sapiens chromosome 14 genomic contig, alternate assembly (based on HuRef SCAF_1103279188393A) | 30.2 | 82.8 | 71% | 19 | 100% |
| gi 157696904 NW_001838027.1 | Homo sapiens chromosome 11 genomic contig, alternate assembly (based on HuRef SCAF_1103279184614) | 30.2 | 56.5 | 90% | 19 | 100% |
| gi 51464027 NT_022517.17 | Homo sapiens chromosome 3 genomic contig, reference assembly | 30.2 | 480 | 100% | 19 | 100% |
| gi 51465675 NT_007592.14 | Homo sapiens chromosome 6 genomic contig, reference assembly | 30.2 | 434 | 100% | 19 | 100% |
| gi 51468880 NT_033927.7 | Homo sapiens chromosome 11 genomic contig, reference assembly | 30.2 | 112 | 90% | 19 | 100% |
| gi 51493278 NT_026437.11 | Homo sapiens chromosome 14 genomic contig, reference assembly | 30.2 | 327 | 100% | 19 | 100% |
| gi 51464897 NT_006576.15 | Homo sapiens chromosome 5 genomic contig, reference assembly | 30.2 | 351 | 90% | 19 | 100% |
| gi 51467290 NT_035014.4 | Homo sapiens chromosome 9 genomic contig, reference assembly | 30.2 | 30.2 | 71% | 19 | 100% |
| gi 88953465 NT_022171.14 | Homo sapiens chromosome 2 genomic contig, reference assembly | 30.2 | 222 | 95% | 19 | 100% |
| gi 89061340 NT_011903.12 | Homo sapiens chromosome Y genomic contig, reference assembly | 30.2 | 135 | 85% | 19 | 100% |
| gi 88966845 NT_005612.15 | Homo sapiens chromosome 3 genomic contig, reference assembly | 30.2 | 668 | 100% | 19 | 100% |
| gi 51463895 NT_022459.14 | Homo sapiens chromosome 3 genomic contig, reference assembly | 30.2 | 84.7 | 80% | 19 | 100% |
| gi 29801560 NT_011295.10 | Homo sapiens chromosome 19 genomic contig, reference assembly | 30.2 | 244 | 95% | 19 | 100% |
| gi 51473102 NT_010498.15 | Homo sapiens chromosome 16 genomic contig, reference assembly | 30.2 | 432 | 100% | 19 | 100% |
| gi 88943682 NT_004487.18 | Homo sapiens chromosome 1 genomic contig, reference assembly | 30.2 | 454 | 100% | 19 | 100% |
| gi 37552484 NT_023736.16 | Homo sapiens chromosome 8 genomic contig, reference assembly | 30.2 | 56.5 | 85% | 19 | 100% |
| gi 51470970 NT_009237.17 | Homo sapiens chromosome 11 genomic contig, reference | 30.2 | 478 | 100% | 19 | 100% |

| | | assembly | EXHIBIT 5 | | | | |
|-----------------------------|--|----------------|-----------|------|-----|------|------|
| gi | accession | USSN_107738413 | 30.2 | 56.5 | 80% | 19 | 100% |
| gi 89024890 NT_007819.16 | Homo sapiens chromosome 7 genomic contig, reference assembly | | | | | | |
| gi 88952973 NT_022221.12 | Homo sapiens chromosome 2 genomic contig, reference assembly | 30.2 | 482 | 100% | 19 | 100% | |
| gi 89059027 NT_011520.11 | Homo sapiens chromosome 22 genomic contig, reference assembly | 30.2 | 482 | 100% | 19 | 100% | |
| gi 37540936 NT_010194.15 | Homo sapiens chromosome 15 genomic contig, reference assembly | 30.2 | 432 | 100% | 19 | 100% | |
| gi 51475294 NT_011512.10 | Homo sapiens chromosome 21 genomic contig, reference assembly | 30.2 | 274 | 100% | 19 | 100% | |
| gi 88942921 NT_032977.8 | Homo sapiens chromosome 1 genomic contig, reference assembly | 30.2 | 587 | 100% | 19 | 100% | |
| gi 51475129 NT_011362.9 | Homo sapiens chromosome 20 genomic contig, reference assembly | 30.2 | 137 | 100% | 19 | 100% | |
| gi 51493354 NT_010859.14 | Homo sapiens chromosome 18 genomic contig, reference assembly | 30.2 | 191 | 90% | 19 | 100% | |
| gi 51467897 NT_030059.12 | Homo sapiens chromosome 10 genomic contig, reference assembly | 30.2 | 456 | 95% | 19 | 100% | |
| gi 157698021 NW_001842414.1 | Homo sapiens chromosome X genomic contig, alternate assembly (based on HuRef SCAF_1103279188251) | 28.2 | 54.5 | 80% | 73 | 100% | |
| gi 157697797 NW_001838459.1 | Homo sapiens chromosome 17 genomic contig, alternate assembly (based on HuRef SCAF_1103279188101) | 28.2 | 28.2 | 66% | 73 | 100% | |
| gi 157697690 NW_001838289.1 | Homo sapiens chromosome 16 genomic contig, alternate assembly (based on HuRef SCAF_1103279188406a) | 28.2 | 28.2 | 66% | 73 | 100% | |
| gi 157696440 NW_001838879.1 | Homo sapiens chromosome 3 genomic contig, alternate assembly (based on HuRef SCAF_1103279181846) | 28.2 | 28.2 | 66% | 73 | 100% | |
| gi 157696476 NW_001838915.1 | Homo sapiens chromosome 4 genomic contig, alternate assembly (based on HuRef SCAF_1103279188399) | 28.2 | 135 | 71% | 73 | 100% | |
| gi 157812004 NW_001838981.2 | Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279188350) | 28.2 | 133 | 85% | 73 | 100% | |
| gi 157812509 NW_001842412.2 | Homo sapiens chromosome X genomic contig, alternate assembly (based on HuRef SCAF_1103279188343) | 28.2 | 80.6 | 95% | 73 | 100% | |
| gi 157812198 NW_001838073.2 | Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188117) | 28.2 | 54.5 | 66% | 73 | 100% | |
| gi 157697796 NW_001838458.1 | | 28.2 | 54.5 | 76% | 73 | 100% | |

Homo sapiens chromosome 17
genomic contig, alternate
assembly (based on HuRef
SCAF_1103279188205)

USSN|10/739443 on HuRef
SCAF_1103279188205)

EXHIBIT 5

| | | | | | | |
|-----------------------------|--|------|------|------|----|------|
| gi 157696179 NW_001838523.1 | Homo sapiens chromosome 1 genomic contig, alternate assembly (based on HuRef SCAF_1103279188240) | 28.2 | 54.5 | 65% | 73 | 100% |
| gi 157697949 NW_001842359.1 | Homo sapiens chromosome X genomic contig, alternate assembly (based on HuRef SCAF_1103279188171A) | 28.2 | 28.2 | 66% | 73 | 100% |
| gi 157811991 NW_001838953.2 | Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188146) | 28.2 | 159 | 90% | 73 | 100% |
| gi 157696949 NW_001838072.1 | Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279184538) | 28.2 | 28.2 | 66% | 73 | 100% |
| gi 157697497 NW_001838219.1 | Homo sapiens chromosome 15 genomic contig, alternate assembly (based on HuRef SCAF_1103279188391) | 28.2 | 28.2 | 66% | 73 | 100% |
| gi 157811954 NW_001838865.2 | Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188138) | 28.2 | 54.5 | 85% | 73 | 100% |
| gi 157811766 NW_001838579.2 | Homo sapiens chromosome 1 genomic contig, alternate assembly (based on HuRef SCAF_1103279188432) | 28.2 | 212 | 100% | 73 | 100% |
| gi 88998470 NT_025741.14 | Homo sapiens chromosome 6 genomic contig, reference assembly | 28.2 | 430 | 100% | 73 | 100% |
| gi 88972123 NT_037622.5 | Homo sapiens chromosome 4 genomic contig, reference assembly | 28.2 | 54.5 | 66% | 73 | 100% |
| gi 51464299 NT_022778.15 | Homo sapiens chromosome 4 genomic contig, reference assembly | 28.2 | 28.2 | 66% | 73 | 100% |
| gi 89060463 NT_011726.13 | Homo sapiens chromosome X genomic contig, reference assembly | 28.2 | 80.8 | 100% | 73 | 100% |
| gi 51466650 NT_007914.14 | Homo sapiens chromosome 7 genomic contig, reference assembly | 28.2 | 139 | 95% | 73 | 100% |
| gi 37552371 NT_011255.14 | Homo sapiens chromosome 19 genomic contig, reference assembly | 28.2 | 133 | 80% | 73 | 100% |
| gi 89059032 NT_011521.4 | Homo sapiens chromosome 22 genomic contig, reference assembly | 28.2 | 28.2 | 66% | 73 | 100% |
| gi 37551285 NT_034880.3 | Homo sapiens chromosome 6 genomic contig, reference assembly | 28.2 | 109 | 85% | 73 | 100% |
| gi 88954065 NT_005403.16 | Homo sapiens chromosome 2 genomic contig, reference assembly | 28.2 | 454 | 100% | 73 | 100% |

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EXHIBIT 5

Designing or Testing PCR Primers? Try your s

Alignments

>gi|113722118|ref|NM_000372.4|  Homo sapiens tyrosinase (oculocutaneous albinism 1A) mRNA
Length=2082

GENE ID: 7299 TYR | tyrosinase (oculocutaneous albinism 1A) [Homo sapiens]
(Over 100 PubMed links)

Score = 42.1 bits (21), Expect = 0.005
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

Query 1 AATAGGACCTGCCAGTGCTCT 21
Sbjct 338 AATAGGACCTGCCAGTGCTCT 358

>gi|32313592|ref|NM_006418.3|  Homo sapiens olfactomedin 4 (OLFM4), mRNA
Length=2844

GENE ID: 10562 OLFM4 | olfactomedin 4 [Homo sapiens] (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 1.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 5 GGACCTGCCAGTGCTCT 21
Sbjct 242 GGACCTGCCAGTGCTCT 258

>gi|149363684|ref|NM_015325.1|  Homo sapiens KIAA0947 protein (KIAA0947), mRNA
Length=7966

GENE ID: 23379 KIAA0947 | KIAA0947 protein [Homo sapiens]
(10 or fewer PubMed links)

Score = 30.2 bits (15), Expect = 19
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 5 GGACCTGCCAGTGCT 19
Sbjct 5584 GGACCTGCCAGTGCT 5598

>gi|142386366|ref|NM_138392.2|  Homo sapiens SH3KBPI binding protein 1 (SHKBPI), mRNA
Length=2357

GENE ID: 92799 SHKBPI | SH3KBPI binding protein 1 [Homo sapiens]
(10 or fewer PubMed links)

Score = 30.2 bits (15), Expect = 19
Identities = 15/15 (100%), Gaps = 0/15 (0%)

Strand=Plus/Minus

Query 5 GGACCTGCCAGTCCT
Subject 980 GGACCTGCCAGTGCT 966

EXHIBIT 5